

Remarks

Upon entry of the amendments submitted herein, claims 23-82 will be pending. Claims 1-22 have been canceled previously or herein without prejudice or disclaimer. Applicants reserve the right to pursue subject matter encompassed by all canceled claims in one or more continuation or divisional applications. No new matter has been added.

Rejection of claims 23-36, 40-53, 57-66, and 70-79 under 35 U.S.C. § 101

The rejection of claims 23-36, 40-53, 57-66, and 70-79 under 35 U.S.C. § 101 as allegedly not being supported by either a specific and substantial utility or a well established utility was maintained. *See* Paper No. 42005, page 2. In particular, the Examiner maintained the allegation that “the specification fails to provide sufficient objective evidence of any activity for encoded protein” and that “there is no information pertaining to the significance of the percentage homology, e.g. whether there were any conserved motifs that would lead the artisan to accept the protein’s function.” *See Id.* at 3.

Applicants respectfully disagree and traverse.

In the first Office Action mailed April 21, 2005, the Examiner introduced the currently pending utility rejection alleging that “the specification fails to provide sufficient objective evidence of any activity for encoded protein.” *See* Paper No. 92004, page 3, last paragraph. In Applicants response to the first office action, passages from the specification were explicitly identified where an activity for the FcR-V polypeptides was indeed asserted. Specifically, Applicant’s response pointed out that the specification indicates that FcR-V polypeptides are “important in the regulation of the immune and hematopoietic systems and are ‘thought to function as an important trigger of complex immune defense responses’” and “are thought to play a dominant role in type II hypersensitivity reactions.” *See* Response to first Office Action, page 13, second full paragraph. Furthermore, Applicants also identified specific immune system related disorders disclosed in the specification for which the FcR-V polypeptides would be useful in treating¹.

¹ The specification teaches that the FcR-V polypeptides are useful for the diagnosis or treatment of specific immune system-related disorders, including “immune-complex related inflammatory diseases such as rheumatoid arthritis, systemic lupus erythmatosis, autoimmune hemolytic anemia, thrombocytopenia and IgG- or IgE-mediated inflammation, anaphylaxis, allergy” *See, e.g.*, page 60, paragraph 0135.

Applicants provided explicit evidence from the specification in their previous response showing a specific biological role for the FcR-V polypeptides (i.e., regulation of the immune and hematopoietic systems) and correlated this role to a specific group of immune system-related disorders. Thus, the specific, substantial, and credible elements under 35 U.S.C. § 101 were met in that such a correlation between the biological activity and the asserted use in specific disease conditions would be, more likely than not, sufficient to convince one of skill in the art of the usefulness of the FcR-V protein. Therefore, Applicants have provided evidence of a specific, substantial, and credible utility and have clearly met their burden in rebutting the *prima facie* assertion of lack of utility. *See*, M.P.E.P. 2107 (II)(3)(i).

The Examiner also alleged in the first office action response that “there is no information pertaining to the significance of the percentage of homology, e.g. whether there were any conserved motifs that would [have] led the artisan to accept the protein’s function.” *See*, Paper No. 92004, page 4. In response, Applicants pointed to specific locations in the specification that disclosed and discussed the importance of the conserved domains between FcR-V and the Fc- γ 2 receptor, as well as shared conserved domains between the well-established family of FcR receptors. *See*, Response to first Office Action, page 14, first full paragraph. *See also*, specification pages 4 and 5, paragraph 0012; page 19, paragraphs 0038-0039; and Figure 14.

Additionally, Applicants pointed to the reference by Raghavan *et al.*, cited in the specification, which discloses that “receptors for the Fc domain of immunoglobulins play an important role in immune defense” and the “biological responses elicited [by Fc receptors] include antibody-dependent, cell-mediated cytotoxicity, phagocytosis, release of inflammatory mediators, and regulation of lymphocyte proliferation and differentiation. *See Id.* at page 19, paragraph 0039. *See also*, Raghavan *et al.*, abstract (previously submitted as reference AG with the IDS filed August 16, 2004). The Raghavan *et al.* reference provides further support for the asserted utility by providing additional discussion on the importance of the conserved domains of Fc receptors, by discussing the involvement of Fc receptors in immune defense, and by providing evidence that the science related to Fc receptors was well-known at the time of earliest filing of the present application.

Applicants assert that the disclosure of both the conserved Fc receptor domains of the FcR-V polypeptide and the reference by Raghaven *et al.* further support the credibility of the asserted specific, substantial, and well-established utility for the FcR-V polypeptide and the corresponding antibodies of the present invention. More specifically, when presented with the evidence indicating that: 1) Fc receptor involvement in immune defense was well-known; 2) Fc receptors contain hallmark Ig-like conserved domains; and 3) the FcR-V polypeptide of the present application contains all hallmark Ig-like domains of Fc receptors, one of skill in the art would expect that the FcR-V polypeptides, and thus antibodies that bind FcR-V, would be useful in treating and/or diagnosing disorders of the immune system, such as, for example, allergy and inflammation.

Despite the evidence presented by Applicants in response to the first office action and summarized herein above, the Examiner responded by issuing a final utility rejection that is *nearly verbatim* to the utility rejection presented in the first office action. *Compare* Paper No. 92004, page 3, last paragraph to page 5, second full paragraph *and* Paper No. 42005, page 3, first full paragraph to page 5, second full paragraph. Applicants respectfully submit that the response provided by the Examiner is improper. As stated in the M.P.E.P.:

Office personnel are reminded that they must treat as true a statement of fact made by an applicant in relation to an asserted utility, unless countervailing evidence can be provided that shows that one of ordinary skill in the art would have a legitimate basis to doubt the credibility of such a statement.

Therefore,

[i]f the applicant responds to the *prima facie* rejection, the Office personnel should review the original disclosure, any evidence relied upon in establishing the *prima facie* showing, any claim amendments, and any new reasoning or evidence provided by the applicant in support of an asserted specific and substantial credible utility. It is essential for Office personnel to recognize, fully consider and respond to each substantive element of any response to a rejection based on lack of utility.

See M.P.E.P. § 2107(II)(D) (emphasis added).

Moreover, the Examiner's response:

must establish that it is more likely than not that a person of ordinary skill in the art would not consider that any utility asserted by the applicant would be specific and substantial. The *prima facie* showing must contain the following elements: (i) An explanation that clearly sets forth the reasoning used in concluding that the asserted utility for the claimed invention is not both specific and substantial nor well-established; (ii) Support for factual findings relied upon in reaching this conclusion; and (iii) An evaluation of all relevant evidence of record, including utilities taught in the closest prior art.

See Id. at § 2107(II)(C)(1)(i-iii) (emphasis added).

Given that the presently pending Final Office Action is nearly a verbatim copy of the previous action, it is readily apparent that the Examiner has not responded to "each substantive element" provided in Applicant's rebuttal argument as required by the M.P.E.P.. This is most particularly apparent as it relates to the significance of the conserved domains for FcR-V or the cited Raghavan *et al.* reference, both of which are disclosed in the specification. Most importantly, the Examiner has not provided any explanation, support, or evidence regarding why one of skill in the art would not believe the asserted utility disclosed in the specification when: 1) presented with the knowledge that the FcR-V polypeptide contains all hallmark conserved domains of Fc receptors; 2) given the well-established roles and biological functions of Fc receptors discussed in Raghavan; and 3) provided with information showing that the Fc receptor art was well-known at the time of the earliest filing of the present application.

In addition to the evidence and explanations previously provided, Applicants herein also point out that the specification teaches that FcR-V polypeptides are expressed by activated monocytes, primary dendritic cells, and macrophages. *See, e.g.*, page 13, paragraph 0024. Hence, given the homology of FcR-V to immune system regulatory molecules² with the described tissue expression exclusively in cells of the immune system, one of ordinary

² FcR-V contains three pairs of the Ig-like domains in its extracellular domain located around the three pairs of cysteine residues located at positions 33 and 81, 139 and 179, and 228 and 279 of SEQ ID NO:10. The Fc- γ 2 receptor is thought to be important in modulation of the immune and hematopoietic systems. The homology

skill in the art would immediately appreciate that the presently claimed antibodies would be useful in regulating immune system functions.

To corroborate the asserted utility for the FcR-V polypeptide, Applicants previously submitted the post-filing date publication by Tedla *et al.* Applicants provided a sequence alignment showing that the LIR7 polypeptide sequence and the FcR-V polypeptide were identical at amino acid positions -16 to 449. Furthermore, Applicants pointed out that both the LIR7 and FcR-V amino acid sequences have Ig-like domains characteristic of FcRs in addition to short cytoplasmic domains and positively charged arginine residues within their transmembrane domains that are characteristic of activating LIRs. Finally, Applicants disclosed that LIR7 activates immunological and/or inflammatory responses which are well-known to play important roles in host responses to inflammation, allergic diseases and parasitic infections. From this information, Applicants explained that Tedla *et al.* further corroborates the asserted utility that FcR-V polypeptides, and thus, that one of ordinary skill in the art would expect antibodies that bind FcR-V to be useful in treating and/or diagnosing disorders of the immune system, such as allergy and inflammation.

Nonetheless, the Examiner alleges that “the sequence of LIR-7 has been disclosed by Borges *et al.* not by Tedla *et al.*, and that sequence alignment of the claimed SEQ ID NO:10 does not show 100% identity over the referenced polypeptide.” See, Paper No. 42005, page 5 fourth full paragraph. In support of this argument, the Examiner provided the results of a database search from SwissProt_42 database search showing an alignment of 465 amino acids of the FcR-V polypeptide vs. a 482 amino acid sequence.

Applicants respectfully disagree with the Examiner’s conclusion. An analysis of the features section of both the SwissProt_42 analysis provided by the Examiner and the NCBI protein sequence database search for Accession No. Q8N149 (submitted herewith as Exhibit A) reveals that the protein sequence provided by the Examiner actually contains a splice variant at amino acid region 419 to 436. Thus, removal of the splice variant yields a 466 amino acid sequence which was identified by Applicants as LIR7 and which is identical to FcR-V at positions -16 to 449 (SEQ ID NO:10).

between the Fc- γ 2 receptor and FcR-V indicates that FcR-V may also be involved in modulation of the immune and hematopoietic systems. See, *e.g.*, pages 19-20, paragraph 0039.

As further evidence that LIR7 is the 466 amino acid sequence previously aligned with FcR-V, Applicants provide herewith the results of a BLAST of the NCBI refseq_human_aa database. The BLAST was performed with the FcR-V polypeptide sequence and the results show 100% alignment over 465 amino acids with the NCBI protein Accession No. NP_006857.1. *See* BLAST results for alignment gi | 5803068 provided herewith as Exhibit B. An NCBI protein sequence database search result for Accession No. NP_006857.1 (submitted herewith as Exhibit C) identifies this 466 amino acid protein as “leukocyte immunoglobulin-like receptor 7” (i.e., LIR7) (*See* “Features” section). Furthermore, the search results also list as Reference 2 (residues 1 to 466) the Tedla *et al.* reference referred to by Applicants herein above and in the previous office action response to corroborate the asserted utility for the FcR-V polypeptide. Thus, Applicants maintain their assertion that the Tedla *et al.* reference further corroborates the asserted utility of the present invention.

Furthermore, the Ig-like domains characteristic of the Fc receptors and the short cytoplasmic domains and positively charged arginine residues within the transmembrane domains, which are characteristic of activating LIRs, are identical between FcR-V and LIR7. Given the that these domains were well-known as significant contributors to the FcR protein’s biological function and given the well-established involvement of FcR proteins in immune responses, one of skill in the art would more likely than not find the asserted utility of the present invention to be specific, substantial, and credible.

Finally, while the Examiner’s concedes that “Tedla et al., further teach that LIR7 may have a possible function in tempering Th2 cell dependent inflammatory response” the Examiner alleges that there “is no recitation of FcR-V polypeptide or possible function of said polypeptide in inflammatory response.” *See*, Paper No. 42005, page 5, fourth full paragraph.

Initially, Applicants assert that the FcR-V polypeptides, and thus, antibodies that bind FcR-V, are useful in treating and/or diagnosing disorders of the immune system, such as allergy and inflammation. As pointed out in the response to the first office action, the specification teaches that the FcR-V polypeptides, which are important in the regulation of the immune and hematopoietic systems, are “thought to function as an important trigger of complex immune defense responses including phagocytosis, antibody-dependent cellular

cytotoxicity, and release of inflammatory mediators” and “appear to play a role in an early step in type II hypersensitivity reactions.” *See*, specification, page 16, paragraph 0032. Additionally, the specification teaches that the FcR-V polypeptides are useful for the diagnosis and/or treatment of specific immune system-related disorders, including

immune-complex related inflammatory diseases such as rheumatoid arthritis, systemic lupus erythmatosis, autoimmune hemolytic anemia, thrombocytopenia and IgG- or IgE-mediated inflammation, anaphylaxis, allergy

See, e.g., page 60, paragraph 0135. Therefore, the specification clearly provides sufficient utility for the FcR-V polypeptide in immune system disorders.

In view of the evidence presented in the response to the first office action and summarized herein, Applicants assert that the totality of the record shows that the asserted utility is well-established, specific, substantial, and credible and therefore the rejection under 35 U.S.C. §101 should be withdrawn. Furthermore, the above evidence and explanations clearly show that the claimed invention has at least one or more patentable utilities. Therefore, Applicants respectfully submit that the rejection of claims 23-36, 40-53, 57-66, and 70-79 under 35 U.S.C. §101 has been obviated and respectfully request that the rejection of the claims be reconsidered and withdrawn.

Rejection of claims 23-36, 40-53, 57-66, and 70-79 under 35 U.S.C. § 112, first paragraph

The rejection of claims 23-36, 40-53, 57-66, and 70-79 under 35 U.S.C. § 112, first paragraph, is maintained based on the premise that “since the claimed invention is not supported by either a specific and substantial, asserted utility or a well established utility for the reasons set forth in the rejection under 35 USC § 101 above, one skilled in the art clearly would not know how to use the claimed invention.” *See*, Paper No. 42005, page 6, item 8.

Applicants respectfully disagree and traverse.

Applicants respectfully submit that, as explained above, claims 23-36, 40-53, 57-66, and 70-79 are supported by specific, substantial, and/or well-established utilities. Hence, in view of the present application’s disclosure and the state of the art as of its earliest filing date, Applicants submit that a person having ordinary skill in the art would certainly know how to use the claimed invention. Accordingly, Applicants respectfully request the rejection of

pending claims 23-36, 40-53, 57-66, and 70-79 under 35 U.S.C. § 112, first paragraph, be reconsidered and withdrawn.

Rejection of Claims 57-66 and 70-79 under 35 U.S.C. § 112, first paragraph

The rejection of claims 57-66 and 70-79 under 35 U.S.C. § 112, first paragraph, is maintained for allegedly “containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.”

See, Paper No. 42005, page 6-7, item 9. In particular, it is asserted that:

Applicant mistakenly assumes that the disclosure of “cell expressing FcR-V” is an equivalent of “FcR-V protein expressed on the surface of a cell”. The genus of “Cells expressing FcR-V” reads on soluble FcR-V and membrane-bound FcR-V, while subgenus “FcR-V protein expressed on the surface of a cell” reads only on a membrane-bound form of FcR-V.

See Id. at page 7, item 12, third full paragraph.

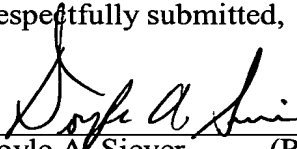
In response, Applicants have herein amended independent claims 57 and 70 to read “An isolated antibody or fragment thereof that specifically binds a FcR-V protein expressed from a cell...”. Support for this amendment can be found, for example, at page 2, paragraph 0006; and, pages 8-11, paragraph 0017. Accordingly, the rejection to claims 57-66 and 70-79 has been obviated. Thus, Applicants respectfully request that the Examiner’s rejection of claims 57-66 and 70-79 under 35 U.S.C. § 112, first paragraph be reconsidered and withdrawn.

Conclusion

Applicants respectfully request that the above-made amendments and remarks be entered and made of record in the file history of the instant application. The Examiner is invited to call the undersigned at the phone number provided below if any further action by Applicant would expedite the examination of this application. If there are any fees due in connection with the filing of this paper, please charge the fees to our Deposit Account No. 08-3425.



Date: 7/21/2005

Respectfully submitted,


Doyle A. Siever (Reg. No. 47,088)
Agent for Applicants

Human Genome Sciences, Inc.
14200 Shady Grove Road
Rockville, Maryland 20850
(301) 354-3932 (Phone)

MJP/DAS/PF/ba

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Range: from to Features: ☐ SNP ☐ CDD ☒ MGC ☐ HPRD ☐ STS

☐ 1: [Q8N149](#). Reports Leukocyte immunog...[gi:37537906]

[BLink](#), [Conserved Domains](#), [Links](#)

LOCUS Q8N149 483 aa linear PRI 01-MAY-2005

DEFINITION Leukocyte immunoglobulin-like receptor subfamily A member 2 precursor (Leukocyte immunoglobulin like receptor 7) (LIR-7) (Immunoglobulin-like transcript 1) (ILT-1) (CD85h antigen).

ACCESSION Q8N149

VERSION Q8N149 GI:37537906

DBSOURCE swissprot: locus LIRA2_HUMAN, accession [Q8N149](#);
class: standard.
extra accessions: O75020, created: Oct 10, 2003.
sequence updated: Oct 10, 2003.
annotation updated: May 1, 2005.
xrefs: [AF025531.1](#), [AAB87665.1](#), [BC017412.1](#), [AAH17412.1](#), [BC027916.1](#), [AAH27916.1](#)
xrefs (non-sequence databases): [HSSPQ8NHL6](#), [EnsembleNSG00000187095](#), [GenewHGNC:6603](#), [MIM 604812](#), [GO0003823](#), [GO0004872](#), [GO0006952](#), [GO0007165](#), [InterProIPR003599](#), [InterProIPR007110](#), [PfamPF00047](#), [SMARTSM00409](#), [PROSITEPS50835](#)

KEYWORDS Alternative splicing; Antigen; Glycoprotein; Immune response; Immunoglobulin domain; Multigene family; Polymorphism; Receptor; Repeat; Signal; Transmembrane.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (residues 1 to 483)

AUTHORS Borges, L., Hsu, M.L., Fanger, N., Kubin, M. and Cosman, D.

TITLE A family of human lymphoid and myeloid Ig-like receptors, some of which bind to MHC class I molecules

JOURNAL J. Immunol. 159 (11), 5192-5196 (1997)

PUBMED [9548455](#)

REMARK NUCLEOTIDE SEQUENCE (ISOFORM 1), AND TISSUE SPECIFICITY.
TISSUE=Peripheral blood leukocytes

REFERENCE 2 (residues 1 to 483)

AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnierch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

CONSRMT Mammalian Gene Collection Program Team

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

PUBMED [12477932](#)

REMARK NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).
 TISSUE=Lung, and Pancreas
 COMMENT [FUNCTION] May act as receptor for class I MHC antigens.
 [SUBCELLULAR LOCATION] Type I membrane protein.
 [ALTERNATIVE PRODUCTS] Event=Alternative splicing; Named isoforms=2; Name=1; IsoId=Q8N149-1; Sequence=Displayed; Name=2; IsoId=Q8N149-2; Sequence=VSP_008455; Note=No experimental confirmation available.
 [TISSUE SPECIFICITY] Expression levels are very low or not detectable on monocytes, T-cells, B-cells, dendritic cells and natural killer (NK) cells.
 [SIMILARITY] Contains 4 immunoglobulin-like C2-type domains.

FEATURES Location/Qualifiers

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 /db_xref="taxon:9606"

gene 1..483
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Protein 1..483
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ORIGIN

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481 agr

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Feb 9 2005 14:31:10

BLAST Results for Result 4416111

BLAST results for sequence
PF363-FcRV

Accession numbers are hotlinked to Entrez at NCBI

The description is hotlinked to the alignment, further down the page

BLASTP 2.0MP-WashU [15-Jun-2000] [sol7-ultra-L64 12:00:28 20-Jun-2000]

Copyright (C) 1996-2000 Washington University, Saint Louis, Missouri USA.
All Rights Reserved.Reference: Gish, W. (1996-2000) <http://blast.wustl.edu>Query= PF363-FcRV
(514 letters)Database: /usr/ncbi/blast/db/refseq_human_aa
28,066 sequences; 14,072,078 total letters.

Searching....10....20....30....40....50....60....70....80....90....100% done

Sequences producing High-scoring Segment Pairs:			High Score	Smallest Sum Probability P(N)	N
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gi 5031911	ref NP_005865.1	leukocyte immunoglobulin-lik...	1749	1.6e-183	2
gi 5729927	ref NP_006660.1	leukocyte immunoglobulin-lik...	1759	2.2e-182	1
gi 31543056	ref NP_006856.2	leukocyte immunoglobulin-lik...	1756	4.7e-182	1
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gi 5803060	ref NP_006855.1	leukocyte immunoglobulin-lik...	1493	3.5e-154	1
gi 47519953	ref NP_036408.3	leukocyte immunoglobulin-lik...	1474	3.6e-152	1
gi 5803070	ref NP_006831.1	leukocyte immunoglobulin-lik...	1330	3.0e-139	2
gi 13399320	ref NP_077293.1	leukocyte immunoglobulin-lik...	884	3.1e-101	2
gi 32895361	ref NP_870994.1	leukocyte Ig-like receptor 9...	637	1.8e-63	1
gi 32490553	ref NP_067073.1	leukocyte Ig-like receptor 9...	636	2.3e-63	1
gi 46488946	ref NP_703144.2	killer cell immunoglobulin-l...	579	2.5e-57	1
gi 5803052	ref NP_006728.1	killer cell immunoglobulin-l...	555	8.7e-55	1
gi 32895365	ref NP_871715.1	leukocyte Ig-like receptor 9...	544	1.3e-53	1
gi 21314641	ref NP_006838.2	leukocyte immunoglobulin-lik...	543	1.6e-53	1
gi 32895363	ref NP_871714.1	leukocyte Ig-like receptor 9...	543	1.6e-53	1
gi 7019441	ref NP_037421.1	killer cell immunoglobulin-l...	538	5.5e-53	1
gi 45505167	ref NP_001546.2	immunoglobulin superfamily, ...	545	1.8e-52	1
gi 37574620	ref NP_057447.3	glycoprotein VI (platelet); ...	437	2.8e-42	1
gi 41208929	ref XP_372748.1	similar to 1060P11.3 (killer...	433	7.3e-42	1
gi 41151816	ref XP_373336.1	similar to 1060P11.3 (killer...	430	1.5e-41	1
gi 7705568	ref NP_056952.1	killer cell immunoglobulin-l...	423	8.4e-41	1
gi 6912472	ref NP_036444.1	killer cell immunoglobulin-l...	417	3.6e-40	1
gi 7657273	ref NP_055034.1	killer cell immunoglobulin-l...	409	2.6e-39	1
gi 7657271	ref NP_055033.1	killer cell immunoglobulin-l...	401	1.8e-38	1
gi 4758692	ref NP_004820.1	natural cytotoxicity trigger...	340	2.0e-37	2
gi 7657277	ref NP_055327.1	killer cell immunoglobulin-l...	385	8.9e-37	1
gi 11968154	ref NP_065396.1	killer cell immunoglobulin-l...	382	1.9e-36	1
gi 7657279	ref NP_055328.1	killer cell immunoglobulin-l...	369	3.8e-36	2
gi 6912474	ref NP_036445.1	killer cell immunoglobulin-l...	375	1.0e-35	1
gi 31982878	ref NP_002246.3	killer cell immunoglobulin-l...	363	1.9e-34	1
gi 19743857	ref NP_579803.1	Fc alpha receptor isoform b ...	274	3.2e-33	2
gi 19743871	ref NP_579813.1	Fc alpha receptor isoform i ...	345	2.1e-32	1
gi 4503673	ref NP_001991.1	Fc alpha receptor isoform a ...	342	4.8e-32	1
gi 45580713	ref NP_570127.2	osteoclast-associated recept...	331	9.2e-31	1
gi 19557664	ref NP_573398.1	osteoclast-associated recept...	330	1.2e-30	1
gi 19557668	ref NP_573399.1	osteoclast-associated recept...	329	1.6e-30	1
gi 19743861	ref NP_579806.1	Fc alpha receptor isoform d;...	310	2.2e-28	1
gi 19743869	ref NP_579812.1	Fc alpha receptor isoform h;...	227	5.5e-28	2
gi 19743873	ref NP_579814.1	Fc alpha receptor isoform j;...	298	4.9e-27	1
gi 46397359	ref NP_036446.2	killer cell immunoglobulin-l...	286	1.0e-25	1
gi 46397357	ref NP_839942.2	killer cell immunoglobulin-l...	286	1.0e-25	1
gi 45580719	ref NP_996554.1	osteoclast-associated recept...	271	4.7e-24	1
gi 19743867	ref NP_579811.1	Fc alpha receptor isoform g;...	264	2.8e-23	1

gi 45580717	ref NP_996553.1	osteoclast-associated recept...	234	5.3e-20	1
gi 21071030	ref NP_570602.2	alpha 1B-glycoprotein [Homo ...	241	1.5e-18	1
gi 33589850	ref NP_055326.2	killer cell immunoglobulin-l...	214	7.9e-18	1
gi 19743865	ref NP_579808.1	Fc alpha receptor isoform f;...	211	1.7e-17	1
gi 10947103	ref NP_067154.1	leukocyte-associated Ig-like...	209	2.8e-17	1

HSP Alignment Overview			Seq Length
ID			
	1-----514		
gi 5803068	----->		466
gi 5803066	----->		489
gi 5031911	----->		598
gi 5729927	----->		650
gi 31543056	----->		439
gi 13324690	----->		464
gi 5803060	----->		631
gi 47519953	----->		499
gi 5803070	----->		590
	1-----514		

WARNING: Descriptions of 92 database sequences were not reported due to the limiting value of parameter V = 50.

>gi|5803068 ref|NP_006857.1| leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2; leukocyte immunoglobulin-like receptor 7 [Homo sapiens]
Length = 466

Score = 2489 (881.2 bits), Expect = 9.9e-260, P = 9.9e-260
Identities = 465/465 (100%), Positives = 465/465 (100%)

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Query:   1 MTPILTVLICLGLSLGPRTHVQAGHLPKPTLWAEPGSVIIQGSFVTLRCQGSQAEEYHL 60
          MTPILTVLICLGLSLGPRTHVQAGHLPKPTLWAEPGSVIIQGSFVTLRCQGSQAEEYHL
Sbjct:   1 MTPILTVLICLGLSLGPRTHVQAGHLPKPTLWAEPGSVIIQGSFVTLRCQGSQAEEYHL 60

Query:   61 YRENKSASWVRRIQEPGKNGQFPISITWEHAGRYHCQYYSHNHSSEYSDPLELVVTGAY 120
          YRENKSASWVRRIQEPGKNGQFPISITWEHAGRYHCQYYSHNHSSEYSDPLELVVTGAY
Sbjct:   61 YRENKSASWVRRIQEPGKNGQFPISITWEHAGRYHCQYYSHNHSSEYSDPLELVVTGAY 120

Query:   121 SKPTLSALPSPVVTLGGNVTLQCVSQVAFDGFILCKEGEDEHPQRLNSHSHARGWSWAIF 180
          SKPTLSALPSPVVTLGGNVTLQCVSQVAFDGFILCKEGEDEHPQRLNSHSHARGWSWAIF
Sbjct:   121 SKPTLSALPSPVVTLGGNVTLQCVSQVAFDGFILCKEGEDEHPQRLNSHSHARGWSWAIF 180

Query:   181 SVGPVSPSRRWSYRCYAYDSNSPYVWSLPSDLELLVPGVSKKPSLSVQPGPMVAPGESL 240
          SVGPVSPSRRWSYRCYAYDSNSPYVWSLPSDLELLVPGVSKKPSLSVQPGPMVAPGESL
Sbjct:   181 SVGPVSPSRRWSYRCYAYDSNSPYVWSLPSDLELLVPGVSKKPSLSVQPGPMVAPGESL 240

Query:   241 TLQCVSDVGYDRFVLYKEGERDFLQRPGWQPQAGLSQANFTLGPVSPSHGGQYRCYSAHN 300
          TLQCVSDVGYDRFVLYKEGERDFLQRPGWQPQAGLSQANFTLGPVSPSHGGQYRCYSAHN
Sbjct:   241 TLQCVSDVGYDRFVLYKEGERDFLQRPGWQPQAGLSQANFTLGPVSPSHGGQYRCYSAHN 300

Query:   301 LSSEWSAPSDPLDILITGQFYDRPSLSVQPVPTVAPGKNVTLLCQSRGQFHTFLLTKEGA 360
          LSSEWSAPSDPLDILITGQFYDRPSLSVQPVPTVAPGKNVTLLCQSRGQFHTFLLTKEGA
Sbjct:   301 LSSEWSAPSDPLDILITGQFYDRPSLSVQPVPTVAPGKNVTLLCQSRGQFHTFLLTKEGA 360

Query:   361 GHPLHLRSEHQQAQONQAEFRMGPVTSAHVGTYRCYSSLSNPYLLSLPSDPLELVVSAS 420
          GHPLHLRSEHQQAQONQAEFRMGPVTSAHVGTYRCYSSLSNPYLLSLPSDPLELVVSAS
Sbjct:   361 GHPLHLRSEHQQAQONQAEFRMGPVTSAHVGTYRCYSSLSNPYLLSLPSDPLELVVSAS 420

Query:   421 LGQHPQDYTVENLIRMGVAGLVLVVLGILLFEAQHSQRSQSLQDAAG 465
          LGQHPQDYTVENLIRMGVAGLVLVVLGILLFEAQHSQRSQSLQDAAG
Sbjct:   421 LGQHPQDYTVENLIRMGVAGLVLVVLGILLFEAQHSQRSQSLQDAAG 465

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>gi|5803066 ref|NP_006854.1| leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1; leukocyte immunoglobulin-like receptor 6 [Homo sapiens]
Length = 489

Score = 1734 (615.5 bits), Expect = 1.2e-196, Sum P(2) = 1.2e-196
Identities = 340/422 (80%), Positives = 355/422 (84%)

Query: 1 MTPILTVLICLGLSLGPRTHVQAGHLPKPTLWAEPGSVIIQGSFVTLRCQGSQAEEYHL 60
 Sbjct: 1 MTPIVTVLICLRLSLGPRTHVQAGTLPKPTLWAEPGSVITQGSFVTLWCQGIETQEYRL 60

Query: 61 YRENKSASWVRRI-QEPGKNGQFFIPISITWEHAGRYHCQYYSHNHS-SEYSDPLELVVTG 118
 YRE K+A W+ RI QE K GQFFIPISITWEH GRY C Y SH SE SDPLELVVTG
 Sbjct: 61 YREKKTAPWITRIPQEIVKKGQFFIPISITWEHTGRYRCFYGSHTAGWSEPSDPLELVVTG 120

Query: 119 AYSKPTLSALPSPVVTLGGNVTLCVSVQVAFDGFILCKEGEDEHPQRLNSHSHARGWSWA 178
 AY KPTLSALPSPVVT GGNVTLCVSVQVAF FILCKEGEDEHPQ LNS GWS A
 Sbjct: 121 AYIKPTLSALPSPVVTSGGNVTLHCVSQVAFGSFILCKEGEDEHPQCLNSQPRTHGWSRA 180

Query: 179 IFSVGPVSPSRRWSYRCYAYDSNSPYVWSLPSDLELLVPGVSKKPSLSVQPGPMVAPGE 238
 IFSVGPVSPSRRWSYRCYAYDSNSP+VWSLPSDLELLV GVSKKPSLSVQPGP+VAPGE
 Sbjct: 181 IFSVGPVSPSRRWSYRCYAYDSNSPHVWSLPSDLELLVVGVSKKPSLSVQPGPIVAPGE 240

Query: 239 SLTLQCVSDVGYDRFVLYKEGERDFLQRPQAGLSQANFTLGPVSPSHGGQYRCYSA 298
 SLTLQCVSDV YDRFVLYKEGERDFLQ PG QPQAGLSQANFTLGPVS S+GGQYRC A
 Sbjct: 241 SLTLQCVSDVSYDRFVLYKEGERDFLQLPQPQAGLSQANFTLGPVSRSYGGQYRCSCA 300

Query: 299 HNLSSSEWSAPSDPLDILITGQFYDRPSLSVQPVPTVAPGKNVTLLCQSPGQFHTFLLTKE 359
 +NLSSEWSAPSDPLDILI GQF RP +SV P PTVA G+NVTLLCQS G FHTFLLTK
 Sbjct: 301 YNLSSEWSAPSDPLDILIAGQFRGRPFISVHPGPTVASGENVTLLCQSWGPFHTFLLTKA 360

Query: 359 GAGHPPLHLRSEHQAAQQAQAEFRMGPVTSAHVGTYRCYSSLSNPYLLSLPSDPLELVVS 418
 GA PL LRS H+ + QAEF M PV TSAH GTYRCY SLSSNPYLLS PSD LEL+VS
 Sbjct: 361 GAADAPLRLRSIHEYPKYQAEFMPSPVTSAHSGTYRCYSGLSNPYLLSHPSDLELMVS 420

Query: 419 AS 420
 +
 Sbjct: 421 GA 422

Score = 477 (173.0 bits), Expect = 6.7e-64, Sum P(2) = 6.7e-64
 Identities = 126/321 (39%), Positives = 177/321 (55%)

Query: 111 PLELVVTGAYSKPTLSALPSPVVTLGGNVTLCVSVQVAFDGFILCKEGEDEHP--QRLNS 168
 P V G KPTL A P V+T G VTL C + + L +E + P R+
 Sbjct: 17 PRTHVQAGTLPKPTLWAEPGSVITQGSFVTLWCQGIETQEYRLYREKTA-PWITRIPQ 75

Query: 169 HSHARGWSWAIFSVPVSPSRRWSYRCYAYDSNSPYVWSLPSDLELLVPGVSKKPSLSV 228
 +G F + ++ YRC+ Y S++ WS PSD LEL+V G KP+LS
 Sbjct: 76 EIVKKGQ----FPIPSITWEHTGRYRCF-YGSHTAG-WSEPSDPLELVVTGAYIKPTLSA 129

Query: 229 QPGPMVAPGESLTLQCVSDVGYDRFVLYKEGERDFLQRPQWQPQA-GLSQANFTLGPVSP 287
 P P+V G ++TL CVS V + F+L KEGE + Q QP+ G S+A F++GPVSP
 Sbjct: 130 LPSPVVTSGGNVTLHCVSQVAFGSFILCKEGEDEHPQCLNSQPRTHGWSRAIFSVPVSP 189

Query: 288 SHGGQYRCYSAHNLSE-WSAPSDPLDILITGQFYDRPSLSVQPVPTVAPGKNVTLLCQS 346
 S YRCY+ + S WS PSD L++L+ G +PSLSVQP P VAPG+++TL C S
 Sbjct: 190 SRRWSYRCYAYDSNSPHVWSLPSDLELLVLG-VSKKPSLSVQPGPIVAPGESLTLQCVS 248

Query: 347 RGQFHTFLLTKEGAGHPPLHLRS-EHQAAQQAQAEFRMGPVTSAHVGTYRCYSSLS-SNPY 404
 + F+L KEG L L + QA +QA F +GPV+ ++ G YRC + + S+ +
 Sbjct: 249 DVSYDRFVLYKEGE-RDFLQLPQPQAGLSQANFTLGPVSRSYGGQYRCSGAYNLSSEW 307

Query: 405 LLSLPSDPLELVVSASLGQHP 425
 S PSDPL++++ P
 Sbjct: 308 --SAPSDPLDILIAGQFRGRP 326

Score = 285 (105.4 bits), Expect = 1.4e-38, Sum P(2) = 1.4e-38
 Identities = 71/207 (34%), Positives = 112/207 (54%)

Query: 28 KPTLWAEPGSVIIQGSFVTLRCQGSQAEEYHLYRENKSASWVRRIQEPGKNGQ----- 81
 KP+L +PG ++ G +TL+C + + + LY+E + +Q PG Q
 Sbjct: 225 KPSLSVQPGPIVAPGESLTLQCVSDVSYDRFVLYKEGERDF---LQLPGPQAGLSQA 280

Query: 82 -FPIPSITWEHAGRYHCQYYSHNHSSEYS--DPLELVVTGAY-SKPTLSALPSPVVTLG 136
 F + ++ + G+Y C ++N SSE+S DPL++++ G + +P +S P P V G
 Sbjct: 281 NFTLGPVSRSYGGQYRCSCG-AYNLSSEWSAPSDPLDILIAGQFRGRPFISVHPGPTVASG 339

Query: 137 GNVTLQCVSVQVAFDGFILCKEGEDEHPQRLNS-HSHARGWSWAIFSVPVSPSRRWSYRC 195
 NVTLC S S F F+L K G + P RL S H + + A F + PV+ + +YRC
 Sbjct: 340 ENVTLLCQSWGPFHTFLLTKAGAADAPLRLRSIHEYPK--YQAEFMPSPVTSAHSGTYRC 397

Query: 196 YAYDSNSPYVWSLPSDLELLVPGVSK 222

Y S++PY+ S PSD LEL+V G ++
 Sbjct: 398 YGSLSSNPYLLSHPSDSLMLVSGAAE 424

Score = 182 (69.1 bits), Expect = 1.2e-196, Sum P(2) = 1.2e-196
 Identities = 36/37 (97%), Positives = 37/37 (100%)

Query: 424 HPQDYTVENLIRMGVAGLVVLVGLLFEAQHSQRSL 460
 HPQDYTVENLIRMG+AGLVVLVGLLFEAQHSQRSL
 Sbjct: 453 HPQDYTVENLIRMGVAGLVVLVGLLFEAQHSQRSL 489

>gi|5031911 ref|NP_005865.1| leukocyte immunoglobulin-like receptor, subfamily
 B (with TM and ITIM domains), member 2; leukocyte
 immunoglobulin-like receptor 2 [Homo sapiens]
 Length = 598

Score = 1749 (620.7 bits), Expect = 1.6e-183, Sum P(2) = 1.6e-183
 Identities = 340/427 (79%), Positives = 361/427 (84%)

Query: 1 MTPILTVLICLGLSLGPRTHVQAGHLPKPTLWAEFGSVIIQGGSPVTLRCQGSQAEEYHL 60
 MTPILTVLICLGLSLGPRTHVQ G +PKPTLWAEF SVI OGSPVTL COGSL+A+EY L
 Sbjct: 1 MTPIVTVLICLGLSLGPRTHVQGTGTIPKPTLWAEFSDVITQGGSPVTLSCQGSLEAEYRL 60

Query: 61 YRENKSASWVRRIQ-EPGKNGQFPISITWEHAGRYHCQYYSHNHSSEYSDPLELVVTGA 119
 YRE KSASW+ RI+ E KNGQF IPSITWEH GRY CQYYS SE SDPL LV+TGA
 Sbjct: 61 YREKKSASWITRIRPELVKNGQFHIPSITWEHTGRYGCQYYSRARWSELSLPLVLMVTGA 120

Query: 120 YSKPTLSALPSPVVTGNGVTLQCVSQVAFDGFILCKEGEDEHPQRLNSHSHARGWSWAI 179
 Y KPTLSA PSPVVT GG VTLQC SQVAF GFILCKEGEDEHPQ LNS HARG S AI
 Sbjct: 121 YPKPTLSAQSPVVTSGGRVTLQCESQVAFGGFILCKEGEDEHPQCLNSQPHARGSSRAI 180

Query: 180 FSVGPVSPSRRWSYRCYAYDSNSPYVWSLPSDLLELLVPGVSKKPSLSVQPGPMVAPGES 239
 FSVGPVSP+RRWS+RCY YD NSPYVWS PSDLLELLVPGVSKKPSLSVQPGP+VAPGES
 Sbjct: 181 FSVGPVSPNRRWSHRCYGYDLNSPYVWSSPSDLLELLVPGVSKKPSLSVQPGPVVAPGES 240

Query: 240 LTLQCVSDVGYDRFVLYKEGERDLQRPGWQPQAGLSQANFTLGPVSPSHGGQYRCYSAH 299
 LTLQCVSDVGYDRFVLYKEGERD Q PG QPQAGLSQANFTLGPVS S+GGQYRCY A+
 Sbjct: 241 LTLQCVSDVGYDRFVLYKEGERDLRQLPGRQPQAGLSQANFTLGPVSRSYGGQYRCYGAY 300

Query: 300 NLSSEWSAPSDPLDILITGQFYDRPSLSVQPVPTVAPGKNVTLQCQSRGQFHTFLLTKEG 359
 NLSSEWSAPSDPLDILITGQ + P +SVQP PTVA G+NVTLQCQ QFHTFLLTK G
 Sbjct: 301 NLSSEWSAPSDPLDILITGQIHGTPFISVQPGPTVASGENVTLQCQSWRQFHTFLLTKAG 360

Query: 360 AGHPPLHLRSEHQQQNAEFMRGPVTSAHVGTYRCYSSLSNPYLLSLPSDPLELVVSA 419
 A PL LRS H+ + QAEF M PV TSAH GTYRCY SL+S+PYLLS PS+PLELVVS
 Sbjct: 361 AADAPLRLRSIHEYPKYQAEFMPSPVTSAHAGTYRCYGSLSNDPYLLSHPSLELVVSG 420

Query: 420 -SLGQHP 425
 S+G P
 Sbjct: 421 PSMGSSP 427

Score = 479 (173.7 bits), Expect = 1.7e-49, Sum P(2) = 1.7e-49
 Identities = 125/328 (38%), Positives = 172/328 (52%)

Query: 17 PRTHVQAGHLPKPTLWAEFGSVIIQGGSPVTLRCQGSQAEEYHLYRENKSASWVRRIQEP 76
 P V G PKPTL A+P V+ G VTL+C+ + + L +E + +P
 Sbjct: 112 PLVLVMTGAYPKPTLSAQSPVVTSGGRVTLQCESQVAFGGFILCKEGEDEHPQCLNSQP 171




Query: 77 GKNQG----FPIPSITWEHAGRYHCQYYSHNHSSEYSDP---LELVVTGAYSKPTLSALP 129
 G F + ++ + C Y N +S P LEL+V G KP+LS P
 Sbjct: 172 HARGSSRAIFSVGPVSPNRRWSHRCYGYDLNSPYVWSSPSDLLELLVPGVSKKPSLSVQP 231

Query: 130 SPVVTGNGVTLQCVSQVAFDGFILCKEGEDEHPQRLNSHSHARGWSWAI FSVGPVSPSR 189
 PVV G ++TLQCVS V +D F+L KEGE + Q L G S A F++GPVS S
 Sbjct: 232 GPVVAPGESLTLQCVSDVGYDRFVLYKEGERDLRQ-LPGRQPQAGLSQANFTLGPVSRSY 290

Query: 190 RWSYRCY-AYDSNSPYVWSLPSDLLELLVPG-VSKKPSLSVQPGPMVAPGESLTLQCVSD 247
 YRCY AY+ +S WS PSD L++L+ G + P +SVQPGP VA GE++TL C S
 Sbjct: 291 GGQYRCYGAYNLSSE--WSAPSDPLDILITGQIHGTPFISVQPGPTVASGENVTLQCQSW 348

Query: 248 VGYDRFVLYKEGERDLQRPGWQPQAGLSQANFTLGPVSPSHGGQYRCYSAHNLSSEW-- 305
 + F+L K G D R + QA F + PV+ +H G YRCY + N S +
 Sbjct: 349 RQFHTFLLTKAGAADAPLRLRSIHEYPKYQAEFMPSPVTSAHAGTYRCYGSLSN-SDPYLL 407

Query: 306 SAPSDPLDILITGQFYDRPSLSVQPVPT 333

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search for

Limits Preview/Index History Clipboard Details

Range: from to Features: ☐ SNP ☐ CDD ☒ MGC ☐ HPRD ☐ STS

☐ 1: [NP_006857](#). Reports leukocyte immunog...[gi:5803068]

BLink, Conserved
Domains, Links

LOCUS NP_006857 466 aa linear PRI 22-APR-2005
DEFINITION leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 [Homo sapiens].
ACCESSION NP_006857
VERSION NP_006857.1 GI:5803068
DBSOURCE REFSEQ: accession [NM_006866.1](#)
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM [Homo sapiens](#)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (residues 1 to 466)
AUTHORS Sloane,D.E., Tedla,N., Awoniyi,M., Macglashan,D.W. Jr., Borges,L., Austen,K.F. and Arm,J.P.
TITLE Leukocyte immunoglobulin-like receptors: novel innate receptors for human basophil activation and inhibition
JOURNAL Blood 104 (9), 2832-2839 (2004)
PUBMED [15242876](#)
REMARK GeneRIF: Cross-linking of basophil LIR7 resulted in the concentration-dependent net release of histamine and cysteinyl leukotrienes that were maximal at 30 minutes, and of IL-4 that was maximal at 4 hours
REFERENCE 2 (residues 1 to 466)
AUTHORS Tedla,N., Bandeira-Melo,C., Tassinari,P., Sloane,D.E., Samplaski,M., Cosman,D., Borges,L., Weller,P.F. and Arm,J.P.
TITLE Activation of human eosinophils through leukocyte immunoglobulin-like receptor 7
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (3), 1174-1179 (2003)
PUBMED [12529506](#)
REMARK GeneRIF: LIR7 is an activating receptor for eosinophils that elicited the release of cytotoxic granule proteins, de novo lipid mediator generation, and cytokine release through vesicular transport
REFERENCE 3 (residues 1 to 466)
AUTHORS Borges,L., Hsu,M.L., Fanger,N., Kubin,M. and Cosman,D.
TITLE A family of human lymphoid and myeloid Ig-like receptors, some of which bind to MHC class I molecules
JOURNAL J. Immunol. 159 (11), 5192-5196 (1997)
PUBMED [9548455](#)
REFERENCE 4 (residues 1 to 466)
AUTHORS Samaridis,J. and Colonna,M.
TITLE Cloning of novel immunoglobulin superfamily receptors expressed on human myeloid and lymphoid cells: structural evidence for new stimulatory and inhibitory pathways
JOURNAL Eur. J. Immunol. 27 (3), 660-665 (1997)
PUBMED [9079806](#)
REFERENCE 5 (residues 1 to 466)
AUTHORS Rojo,S., Burshtyn,D.N., Long,E.O. and Wagtmann,N.
TITLE Type I transmembrane receptor with inhibitory function in mouse mast cells and NK cells
JOURNAL J. Immunol. 158 (1), 9-12 (1997)
PUBMED [8977169](#)
COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final NCBI review. The reference sequence was derived from [U82275.1](#).

Summary: Leukocyte Ig-like receptors (LIRs) are a family of

immunoreceptors expressed predominantly on monocytes and B cells and at lower levels on dendritic cells and natural killer (NK) cells. All LIRs in subfamily B have an inhibitory function (see, e.g., LILRB1, MIM 604811). LIRs in subfamily A, with short cytoplasmic domains lacking an immunoreceptor tyrosine-based inhibitory motif (ITIM) and with transmembrane regions containing a charged arginine residue, may initiate stimulatory cascades. One member of subfamily A (LILRA3; MIM 604818) lacks a transmembrane region and is presumed to be a soluble receptor. [supplied by OMIM].

FEATURES
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 /map="19q13.4"
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 /note="leukocyte immunoglobulin-like receptor 7"
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 /coded_by="NM_006866.1:88..1488"
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 go_function: antigen binding [goid 0003823] [evidence TAS] [pmid 9548455];
 go_function: receptor activity [goid 0004872] [evidence TAS] [pmid 9548455];
 go_process: immune response [goid 0006955] [evidence IEA];
 go_process: signal transduction [goid 0007165] [evidence TAS] [pmid 9548455]"
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 /db_xref="GeneID:11027"
 /db_xref="MIM:604812"

ORIGIN

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61 yrenksaswv rriqepgkng qfpipsitwe hagryhcqyy shnhsseysd plelvvtgay
121 skptlsalps pvtltggnvt lqcvsqvafd gfilckeged ehqqrlnshs hargwsaif
181 svgpvspsrr wsyrcaayds nsppvslps dllellvpgv skkpslsvqp gpmvapgesl
241 tlqcvsdvgy drfvlykege rdflqrpqwg pqaglsqanf tlgpvspshg ggyrcysahn
301 lssewsapsd pldilitgqf ydrpslsvqp vptvapgknv tllcqsrgqf htflltkaga
361 ghpphlhrse hqaqqnqaef rmgpvtsahv gtyrcyssl snpyllslps dplelvvsas
421 lgqhpqdytv enlirmgvag lvlvvlgill feaqhsqrsl qdaagr

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